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# **Title:** Recent Asian origin of chytrid fungi causing global amphibian declines\*

**Authors:** Simon J. O'Hanlon<sup>1,2\*</sup>, Adrien Rieux<sup>3</sup>, Rhys A. Farrer<sup>1</sup>, Gonçalo M. Rosa<sup>2,4,5</sup>, Bruce Waldman<sup>6</sup>, Arnaud Bataille<sup>6,7</sup>, Tiffany A. Kosch<sup>8,6</sup>, Kris A. Murray<sup>1</sup>, Balázs Brankovics<sup>9,10</sup>, Matteo Fumagalli<sup>11,31</sup>, Michael D. Martin<sup>12,13</sup>, Nathan Wales<sup>13</sup>, Mario Alvarado-Rybak<sup>14</sup>, Kieran A. Bates<sup>1,2</sup>, Lee Berger<sup>8</sup>, Susanne Böll<sup>15</sup>, Lola Brookes<sup>2</sup>, Frances Clare<sup>1,2</sup>, Elodie A. Courtois<sup>16</sup>, Andrew A. Cunningham<sup>2</sup>, Thomas M. Doherty-Bone<sup>17</sup>, Pria Ghosh<sup>1,18</sup>, David J. Gower<sup>19</sup>, William E. Hintz<sup>20</sup>, Jacob Höglund<sup>21</sup>, Thomas S. Jenkinson<sup>22</sup>, Chun-Fu Lin<sup>23</sup>, Anssi Laurila<sup>21</sup>, Adeline Loyau<sup>24,25</sup>, An Martel<sup>26</sup>, Sara Meurling<sup>21</sup>, Claude Miaud<sup>27</sup>, Pete Minting<sup>28</sup>, Frank Pasmans<sup>26</sup>, Dirk Schmeller<sup>24,25</sup>, Benedikt R. Schmidt<sup>29</sup>, Jennifer M. G. Shelton<sup>1</sup>, Lee F. Skerratt<sup>8</sup>, Freya Smith<sup>2,30</sup>, Claudio Soto-Azat<sup>14</sup>, Matteo Spagnoletti<sup>31</sup>, Giulia Tessa<sup>32</sup>, Luís Felipe Toledo<sup>33</sup>, Andrés Valenzuela-Sánchez<sup>34,14</sup>, Ruhan Verster<sup>18</sup>, Judit Vörös<sup>35</sup>, Rebecca J. Webb<sup>8</sup>, Claudia Wierzbicki<sup>1</sup>, Emma Wombwell<sup>2</sup>, Kelly R. Zamudio<sup>36</sup>, David M. Aanensen<sup>37,1</sup>, Timothy Y. James<sup>22</sup>, M. Thomas P. Gilbert<sup>13,12</sup>, Ché Weldon<sup>18</sup>, Jaime Bosch<sup>38</sup>, François Balloux<sup>31†</sup>, Trenton W. J. Garner<sup>2,18,32†</sup>, Matthew C. Fisher<sup>1\*</sup>

## **Affiliations:**

<sup>1</sup> Department of Infectious Disease Epidemiology and MRC Centre for Global Infectious Disease Analysis, School of Public Health, Imperial College London, Norfolk Place, London W2 1PG, UK

<sup>2</sup> Institute of Zoology, Regent's Park, London, NW1 4RY, UK

<sup>3</sup> CIRAD, UMR PVBMT, 97410 St Pierre, Reunion, France <sup>4</sup> Department of Biology, University of Nevada, Reno, Reno NV 89557, USA

<sup>5</sup> Centre for Ecology, Evolution and Environmental Changes (CE3C), Faculdade de Ciências da Universidade de Lisboa, Lisboa, Portugal

<sup>6</sup> Laboratory of Behavioral and Population Ecology, School of Biological Sciences, Seoul National University, Seoul 08826, South Korea

<sup>7</sup> CIRAD, UMR ASTRE, F-34398 Montpellier, France

<sup>8</sup> One Health Research Group, College of Public Health, Medical and Veterinary Sciences, James Cook University, Townsville, Queensland, 4811, Australia

<sup>9</sup> Westerdijk Fungal Biodiversity Institute, Uppsalalaan 8, 3584CT Utrecht, The Netherlands

<sup>10</sup> Institute of Biodiversity and Ecosystem Dynamics, University of Amsterdam, Science Park 904, 1098 XH Amsterdam, The Netherlands

<sup>11</sup> Department of Life Sciences, Silwood Park Campus, Imperial College London, Ascot, UK

<sup>12</sup> Department of Natural History, NTNU University Museum, Norwegian University of Science and Technology (NTNU), Erling Skakkes gate 49, NO-7012 Trondheim, Norway

<sup>13</sup> Centre for GeoGenetics, Natural History Museum of Denmark, University of Copenhagen, Øster Voldgade 5-7, 1350 Copenhagen, Denmark

<sup>14</sup> Centro de Investigación para la Sustentabilidad, Facultad de Ecología y Recursos Naturales, Universidad Andres Bello, Republica 440, Santiago, Chile

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- <sup>15</sup> Agency for Population Ecology and Nature Conservancy, Gerbrunn
- <sup>16</sup> Laboratoire Ecologie, évolution, interactions des systèmes amazoniens (LEEISA), Université de Guyane, CNRS, IFREMER, 97300 Cayenne, French Guiana.
- <sup>17</sup> Conservation Programmes, Royal Zoological Society of Scotland, Edinburgh, UK
- <sup>18</sup> Unit for Environmental Sciences and Management, Private Bag x6001, North-West University, Potchefstroom, 2520, South Africa
- <sup>19</sup> Life Sciences, The Natural History Museum, London SW7 5BD, UK
- <sup>20</sup> Biology Department, University of Victoria, Victoria, BC, V8W 3N5, Canada
- <sup>21</sup> Department of Ecology and Genetics, EBC, Uppsala University. Norbyv. 18D, SE-75236, Uppsala, Sweden
- <sup>22</sup> Department of Ecology and Evolutionary Biology, University of Michigan, Ann Arbor, MI, 48109, USA
- <sup>23</sup> Zoology Division, Endemic Species Research Institute, 1 Ming-shen East Road, Jiji, Nantou 552, Taiwan
- <sup>24</sup> Helmholtz Centre for Environmental Research – UFZ, Department of Conservation Biology, Permoserstrasse 15, 04318 Leipzig, Germany
- <sup>25</sup> EcoLab, Université de Toulouse, CNRS, INPT, UPS, Toulouse, France
- <sup>26</sup> Department of Pathology, Bacteriology and Avian Diseases, Faculty of Veterinary Medicine, Ghent University, Salisburylaan 133, B-9820 Merelbeke, Belgium
- <sup>27</sup> PSL Research University, CEFE UMR 5175, CNRS, Université de Montpellier, Université Paul-Valéry Montpellier, EPHE, Montpellier, France
- <sup>28</sup> Amphibian and Reptile Conservation (ARC) Trust, 655A Christchurch Road, Boscombe, Bournemouth, Dorset, UK, BH1 4AP
- <sup>29</sup> Department of Evolutionary Biology and Environmental Studies, University of Zurich, Winterthurerstrasse 190, 8057 Zurich, Switzerland and Info Fauna Karch, UniMail - Bâtiment G, Bellevaux 51, 2000 Neuchâtel, Switzerland
- <sup>30</sup> National Wildlife Management Centre, APHA, Woodchester Park, Gloucestershire GL10 3UJ, UK
- <sup>31</sup> UCL Genetics Institute, University College London, Gower Street, WC1E 6BT, London, UK
- <sup>32</sup> Non-profit Association Zirichiltaggi - Sardinia Wildlife Conservation, Strada Vicinale Filigheddu 62/C, I-07100 Sassari, Italy
- <sup>33</sup> Laboratório de História Natural de Anfíbios Brasileiros (LaHNAB), Departamento de Biologia Animal, Instituto de Biologia, Unicamp, Campinas, Brazil
- <sup>34</sup> ONG Ranita de Darwin, Nataniel Cox 152, Santiago, Chile
- <sup>35</sup> Collection of Amphibians and Reptiles, Department of Zoology, Hungarian Natural History Museum, Budapest, Baross u. 13., 1088, Hungary
- <sup>36</sup> Department of Ecology and Evolutionary Biology, Cornell University, Ithaca, NY, 14853, USA
- <sup>37</sup> Centre for Genomic Pathogen Surveillance, Wellcome Genome Campus, Cambridgeshire, UK
- <sup>38</sup> Museo Nacional de Ciencias Naturales, CSIC c/ Jose Gutierrez Abascal 2, 28006 Madrid, Spain

\*Corresponding authors. Email: [simon.ohanlon@gmail.com](mailto:simon.ohanlon@gmail.com) and [matthew.fisher@imperial.ac.uk](mailto:matthew.fisher@imperial.ac.uk)

†These authors share an equal contribution

89   **One Sentence Summary:** East Asia is the source of amphibian panzootic chytrid fungi  
90   causing global amphibian declines that have emerged during the 20<sup>th</sup> century  
91



92   **Abstract:**

93   Globalized infectious diseases are causing species declines worldwide but their source often  
94   remains elusive. We use whole-genome sequencing to solve the spatiotemporal origins of the  
95   most devastating panzootic to date, caused by the fungus *Batrachochytrium dendrobatidis*, a  
96   proximate driver of global amphibian declines. We trace the source of *B. dendrobatidis* to the  
97   Korean peninsula where one lineage, *BdASIA-1*, exhibits the genetic hallmarks of an  
98   ancestral population that seeded the panzootic. We date the emergence of this pathogen to the  
99   early 20<sup>th</sup> century coinciding with the global expansion of commercial trade in amphibians  
100   and show that intercontinental transmission is ongoing. Our findings point to East Asia as a  
101   geographic hotspot for *B. dendrobatidis* biodiversity, and the original source of these lineages  
102   that now parasitize amphibians worldwide.

## 103 **Main Text:**

104 Discovery of the amphibian-killing fungus *Batrachochytrium dendrobatidis* (1, 2) was a  
 105 turning point in understanding why amphibian species worldwide are in steep decline.  
 106 Amphibian declines and extinctions had been recorded by herpetologists as early as the  
 107 1970s, but were only recognized at a landmark meeting in 1990 as a global phenomenon  
 108 which could not be explained by environmental changes and anthropogenic factors alone (3).  
 109 The emergence of *B. dendrobatidis* and the disease that it causes, amphibian  
 110 chytridiomycosis, as a causative agent of declines has been documented across six different  
 111 regions: Australia (~1970s and 1990s) (4), Central America (~1970s) (5), South America  
 112 (~1970s and 1980s) (6, 7), the Caribbean islands (~2000s) (8), the North American Sierra  
 113 Nevada (~1980s and 1990s) (9), and the Iberian Peninsula (~1990s) (10). The panzootic has  
 114 been attributed to the emergence of a single *B. dendrobatidis* lineage, known as *BdGPL*  
 115 (Global Panzootic Lineage) (11). However, twenty years after identification of the disease,  
 116 the timing of its worldwide expansion remains unknown and previous estimates for time to  
 117 most recent common ancestor (TMRCA) for *BdGPL* span two orders of magnitude, from 100  
 118 ybp (11) to 26,000 ybp (12). The geographic origin of the pathogen is similarly contested,  
 119 with the source of the disease variously suggested to be Africa (13), North America (14),  
 120 South America (15), Japan (16) and East Asia (17).

## 121 **Global diversity of *B. dendrobatidis***

122 To resolve these inconsistencies, we isolated *B. dendrobatidis* from all the candidate source  
 123 continents and sequenced the genomes of 177 isolates to high depth then combined our data  
 124 with published genomes from three prior studies (11, 12, 18) to generate a globally  
 125 representative panel of 234 isolates (Fig. 1A). This dataset covers all continents from which  
 126 *B. dendrobatidis* has been detected to date, and spans infections of all three extant orders of

Amphibia (Fig. S1 and Table S1). Mapped against the *B. dendrobatidis* reference genome JEL423, our sequencing recovered 586,005 segregating single nucleotide polymorphisms (SNPs). Phylogenetic analysis recovered all previously detected divergent lineages (Fig. 1B and Fig. S2). The previously accepted lineages *BdGPL* (global), *BdCAPE* (African), *BdCH* (European) and *BdBRAZIL* (Brazilian), were all detected (19), but our discovery of a new hyperdiverse lineage in amphibians native to the Korean peninsula (*BdASIA-1*) redefined these lineages and their relationships. The *BdCH* lineage, which was previously thought to be enzootic to Switzerland (11) now groups with the *BdASIA-1* lineage. A second Asian-associated lineage (*BdASIA-2*) was recovered from invasive North American bullfrogs in Korea and is closely related to the lineage that is enzootic to the Brazilian Atlantic forest (*BdBRAZIL*) (20). It was not possible to infer the direction of intercontinental spread between isolates within this lineage so it was named *BdASIA-2/BdBRAZIL*. Conditional on the midpoint rooting of the phylogeny in Fig. 1B, we now define the main diverged lineages as *BdGPL*, *BdCAPE*, *BdASIA-1* (which includes the single *BdCH* isolate) and *BdASIA-2/BdBRAZIL*. Previous phylogenetic relationships developed using the widely used ribosomal intragenic spacer *ITS-1* region do not accurately distinguish *B. dendrobatidis* lineages (Fig. S3) and this likely explains much of the place-of-origin conflict in the literature (15-17).

Pairwise comparisons among isolates within each lineage show that the average number of segregating sites is three-fold greater for *BdASIA-1* than for any other lineage (Fig. 1A and Table 1) and that nucleotide diversity ( $\pi$ ; Fig. S4) is two to four-fold greater. Seven of our eight *BdASIA-1* isolates were recently cultured from wild South Korean frogs while the other came from the pet-trade in Belgium, all of which were aclinical infections. These isolates show that the Korean peninsula is a global centre of *B. dendrobatidis* diversity and that East Asia may contain the ancestral population of *B. dendrobatidis*, as suggested by Bataille *et al*

(17). We investigated this hypothesis further using Bayesian-based haplotype clustering (21) and found the greatest haplotype sharing among isolates within *BdASIA-1* and between *BdASIA-1* and all other lineages. This provides direct genetic evidence that *BdASIA-1* shares more diversity with the global population of *B. dendrobatidis* than any other lineage (Fig. S5). In an independent test of ancestry, we used OrthoMCL (22) to root a *B. dendrobatidis* phylogeny to its closest known relative *B. salamandrivorans* which currently threatens salamanders (23). This tree indicates that the Asian and Brazilian isolates of *B. dendrobatidis* lie outside a clade comprising all other isolates (Fig. S6 and Table S2). To identify the signature of demographic histories across lineages we used Tajima's *D* (24). Genome scans of most lineages showed highly variable positive and negative values of *D* with maxima exhibited by *BdGPL* (-2.6 to +6.2; Fig. 2F), indicating that these lineages (*BdASIA-2/BdBRAZIL*, *BdCAPE* and *BdGPL*) have undergone episodes of population fluctuation, strong natural selection, or both, that are consistent with a history of spatial and host radiations. In striking contrast, *BdASIA-1* shows a flat profile for Tajima's *D* (Fig. 2F) indicating mutation-drift equilibrium likely reflective of pathogen endemism in this region.

### **Dating the emergence of *BdGPL***

The broad range of previous estimates for the TMRCA of *BdGPL* spanning 26,000 years (11, 12) can be explained by two sources of inaccuracy: (1) unaccounted recombination and (2) the application of unrealistic evolutionary rates. To address these, we first interrogated the 178,280 kbp mitochondrial genome (mtDNA), which has high copy number and low rates of recombination compared to the nuclear genome. To resolve the structure of the mtDNA genome we resorted to long-read sequencing using a MinION device (Oxford Nanopore Technologies, Cambridge, UK), which allowed us to describe this molecules unusual configuration; *Batrachochytrium dendrobatidis* carries three linear mitochondrial segments, each having inverted repeats at the termini with conserved mitochondrial genes spread over

two of the segments (Fig. S7). Additionally, we sought regions of the autosomal genome with low rates of recombination to obtain an independent estimate of the TMRCA of *BdGPL*.

Detection of crossover events in the *B. dendrobatidis* autosomal genome (18) using a subset of the isolates in this study revealed a large (1.66Mbp) region of Supercontig\_1.2 in *BdGPL* that exhibits several features that identified it as a recombination ‘coldspot’: (1) a continuous region of reduced Tajima’s *D* (Fig. 2D); (2) sustained high values of  $F_{ST}$  when compared with all other lineages (Fig. 3A); (3) a continuous region of reduced nucleotide diversity ( $\pi$ , Fig. S4) and (4) shared loss-of-heterozygosity (Fig. S8). We expanded sampling to infer the temporal range of pathogen introductions using a broad panel of isolates with known date of isolation ( $n = 184$ , ranging from 1998 to 2016) and whole-genome RNA-baiting to obtain reads from preserved amphibians that had died of chytridiomycosis. We then investigated whether our dataset contained sufficient signal to perform tip-dating inferences by building phylogenetic trees using PhyML (25) (Fig. 2A and 2C) then fitting root-to-tip distances to collection dates both at the whole-tree and within-lineage scales. We observed a positive and significant correlation within *BdGPL* only, for both the mitochondrial and nuclear genomes, demonstrating sufficient temporal signal to perform thorough tip-dating inferences at this evolutionary scale (Fig. 2B and 2D).

Tip-dating in BEAST was used to co-estimate ancestral divergence times and the rate at which mutations accumulate within the *BdGPL* lineage. The mean mitochondrial substitution rate was  $1.01 \times 10^{-6}$  substitutions/site/year (95% highest posterior density (HPD)  $4.29 \times 10^{-7} - 1.62 \times 10^{-6}$ ). The mean nuclear substitution rate was  $7.29 \times 10^{-7}$  substitutions/site/year (95% HPD  $3.41 \times 10^{-7} - 1.14 \times 10^{-6}$ ), which is comparable to a recent report of an evolutionary rate of  $2.4 - 2.6 \times 10^{-6}$  substitutions/site/year for another unicellular yeast, *Saccharomyces cerevisiae* beer strains (26). These estimates are over 300-fold faster than the rate used in a

previous study (12) to obtain a TMRCA of 26,400 years for *BdGPL*. Accordingly, we estimate the ancestor of the amphibian panzootic *BdGPL* originated between 120 and 50 years ago (Fig. 2E), with HPD estimates of 1898 [95% HPD 1809-1941] and 1962 [95% HPD 1859-1988] for the nuclear and mitochondrial dating analyses respectively (Fig. 2F).

We considered an additional calibration approach for the TMRCA of the mitochondrial genome where we included informative priors on nodes around the dates for the first historical descriptions of *BdGPL* detection in Australia (1978), Central America (1972), Sierra de Guadarrama (Europe) (1997), and the Pyrenees (Europe) (2000). We did not include priors for nodes where observed declines have been reported, but where the lineage responsible for those declines is unknown. This mixed dating method based on tips and nodes calibration yielded very similar estimates (TMRCA estimates of 1975 [95% HPD 1939 – 1989] (Fig. S9)), further strengthening our confidence in a recent date of emergence for *BdGPL*. An expansion of *BdGPL* in the 20<sup>th</sup> century coincides with the global expansion in amphibians traded for exotic pets, medical and food purposes (27, 28). Within our phylogeny, we found representatives from all lineages among traded animals (Figs. S10-14), and identified ten events where traded amphibians were infected with non-enzootic isolates (Fig. 4). This finding demonstrates the ongoing failure of international biosecurity despite the listing of *B. dendrobatidis* by the World Organisation for Animal Health (the OIE) in 2008.

### **Hybridisation between recontacting lineages of *B. dendrobatidis***

To determine the extent to which the four main lineages of *B. dendrobatidis* have undergone recent genetic exchange, we used the site-by-site based approach implemented in STRUCTURE (29). Although most isolates could be assigned unambiguously to one of the four main lineages, we identified three hybrid genotypes (Fig. 3B), including one previously reported hybrid (isolate CLFT024/2) (20), and discovered two newly identified hybrids of

*BdGPL* and *BdCAPE* in South Africa. Furthermore, *BdCH* (isolate 0739) appears to be a chimera of multiple lineages that may represent unsampled genomic diversity that resides in East Asia, rather than true hybridisation. These hybrid genomes demonstrate that *B. dendrobatidis* is continuing to exchange haplotypes among lineages when they interact following continental invasions, generating novel genomic diversity. We analysed isolate clustering using principle components analysis on a filtered subset of 3,900 SNPs in linkage equilibrium, revealing an overall population structure that is consistent with our phylogenetic analyses (Fig 3C). In addition, the putatively identified hybrid isolates of *B. dendrobatidis* were shown to fall between main lineage clusters (Fig. 3C) further strengthening our hypothesis of haplotype exchange occurring during secondary contact between lineages.

### **Associations among lineage, virulence and declines**

Genotypic diversification of pathogens is commonly associated with diversification of traits associated with host exploitation (30), and is most commonly measured as the ability to infect a host and to cause disease post-infection. We tested for variation of these two phenotypic traits across four *B. dendrobatidis* lineages by exposing larval and post-metamorphic common toads (*Bufo bufo*). Larvae are highly susceptible to infection but do not die before metamorphosis, in contrast to post-metamorphic juveniles, which are susceptible to infection and fatal chytridiomycosis (31). In tadpoles, both *BdGPL* and *BdASIA-1* were significantly more infectious than *BdCAPE* and *BdCH* (Fig. S15 and Tables S3 & S4). In metamorphs, *BdGPL* was significantly more infectious than the other treatments, compared to the control group, and significantly more lethal in experimental challenge, than the geographically more restricted *BdCAPE*, *BdASIA-1* and *BdCH* (Fig. 2G). We further tested for differences in virulence among lineages by using our global dataset to examine whether chytridiomycosis was non-randomly associated with *B. dendrobatidis* lineage. We detected a significant

difference ( $p < 0.001$ ) in the proportion of isolates associated with chytridiomycosis among the three parental lineages (*BdASIA-1* and *BdASIA-2/BdBRAZIL* were grouped due to low sample sizes), and *post hoc* tests indicated significant excess in virulence in both *BdGPL* and *BdCAPE* lineages relative to the combined *BdASIA-1* and *BdASIA-2/BdBRAZIL* (all  $p < 0.05$ ). However, we did not detect a significant difference between *BdGPL* and *BdCAPE* (Fig. S16 and Table S5). These data suggest that although *BdGPL* is highly virulent, population-level outcomes are also context dependent (32); under some conditions other lineages can also be responsible for lethal amphibian disease and population declines (33).

### **Historical and contemporary implications of panzootic chytridiomycosis**

Our results point to endemism of *B. dendrobatidis* in Asia, out of which multiple panzootic lineages have emerged. These emergent diasporas include the virulent and highly transmissible *BdGPL* which spread during the early 20<sup>th</sup> century via a yet unknown route to infect close to 700 amphibian species out of ~1300 thus far tested (34). With over 7800 amphibian species currently described, the number of affected species is likely to rise. The international trade in amphibians has undoubtedly contributed directly to vectoring this pathogen worldwide (Fig. 4; 35,36), and within our phylogeny we identified many highly supported ( $\geq 90\%$  bootstrap support) clades on short branches that linked isolates collected from wild amphibian populations across different continents (Fig. 4; Fig. S10-S14). However, the role of globalised trade in passively contributing to the spread of this disease cannot be ruled out. It is likely no coincidence that our estimated dates for the emergence of *BdGPL* span the globalisation ‘big bang’, the rapid proliferation in intercontinental trade, capital, and technology that started in the 1820s (37). The recent invasion of Madagascar by Asian common toads hidden within mining equipment (38) demonstrates the capacity for amphibians to escape detection at borders and exemplifies how the unintended anthropogenic



dispersal of amphibians has also likely contributed to the worldwide spread of pathogenic chytrids.

The hyperdiverse hotspot identified in Korea likely represents a fraction of the *Batrachochytrium* genetic diversity in Asia and further sampling across this region is urgently needed because the substantial global trade in Asian amphibians (39) presents a risk of seeding future outbreak lineages. Unique ribosomal DNA haplotypes of *B. dendrobatidis* have been detected in native amphibian species in India (40, 41), Japan (16) and China (42). Although caution should be observed when drawing conclusions about lineages based on short sequence alignments (Fig. S3), other endemic lineages probably remain undetected within Asia. Significantly, the northern European countryside is witnessing the emergence of *B. salamandrivorans*, which also has its origin in Asia. The emergence of *B. salamandrivorans* is linked to the amphibian pet trade (43), and the broad expansion of virulence factors that are found in the genomes of these two pathogens are testament to the evolutionary innovation that has occurred in these Asian *Batrachochytrium* fungi (23). Our findings show that the global trade in amphibians continues to be associated with the translocation of chytrid lineages with panzootic potential. Ultimately, our work confirms that panzootics of emerging fungal diseases in amphibians are caused by ancient patterns of pathogen phylogeography being redrawn as largely unrestricted global trade moves pathogens into new regions, infecting new hosts and igniting disease outbreaks. Within this context, the continued strengthening of transcontinental biosecurity is critical to the survival of amphibian species in the wild (44).

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**Competing interests:** KAM sits on an expert panel at the European Food Safety Authority addressing the risks of importation and spread of the salamander chytrid *Batrachochytrium salamandrivorans*, a species of fungus that is the closest known relative to the pathogen addressed in this manuscript.

**Data availability:** Sequences have been deposited in the National Center for Biotechnology Information (NCBI) Sequence Read Archive (SRA). All sequences are available from NCBI BioProject accession PRJNA413876 (<https://www.ncbi.nlm.nih.gov/bioproject/PRJNA413876>). The supplementary materials contain additional data. Phylogenetic trees are available from TreeBASE, project accession url: <http://purl.org/phylo/treebase/phyloids/study/TB2:S22286>. A browsable version of the phylogeny and metadata in Fig. 1B is accessible at: <https://microreact.org/project/GlobalBd>

## **List of supplementary materials:**

Materials and Methods

Figs. S1 to S15

Tables S1 to S5

Data S1 to S3

References (45-92)

611 **Tables:**

Lineage	Number of Isolates	Total segregating sites	Average pairwise-segregating sites	Total homozygous segregating sites	Average pairwise-homozygous segregating sites	$\pi$	Tajima's $D$
<i>Bd</i> ASIA-1	8	327,996	142,437	108,353	21,716	0.0044	0.2540
<i>Bd</i> ASIA-2 / <i>Bd</i> BRAZIL	12	148,021	51,069	48,722	6,216	0.0018	0.9825
<i>Bd</i> CAPE	24	146,466	38,881	53,884	4,977	0.0016	0.3143
<i>Bd</i> GPL	187	127,770	26,546	68,493	3,101	0.0009	0.9792

612

613 **Table 1.** Comparison of common genetic diversity measures among *Batrachochytrium*614 *dendrobatidis* lineages. Total segregating sites for each lineage include all segregating sites

615 where genotype calls were made in at least half of the isolates. Average pairwise-segregating

616 sites is the average number of sites with different genotypes between all pairs of isolates

617 within a lineage. Total homozygous segregating sites includes all sites within a lineage where

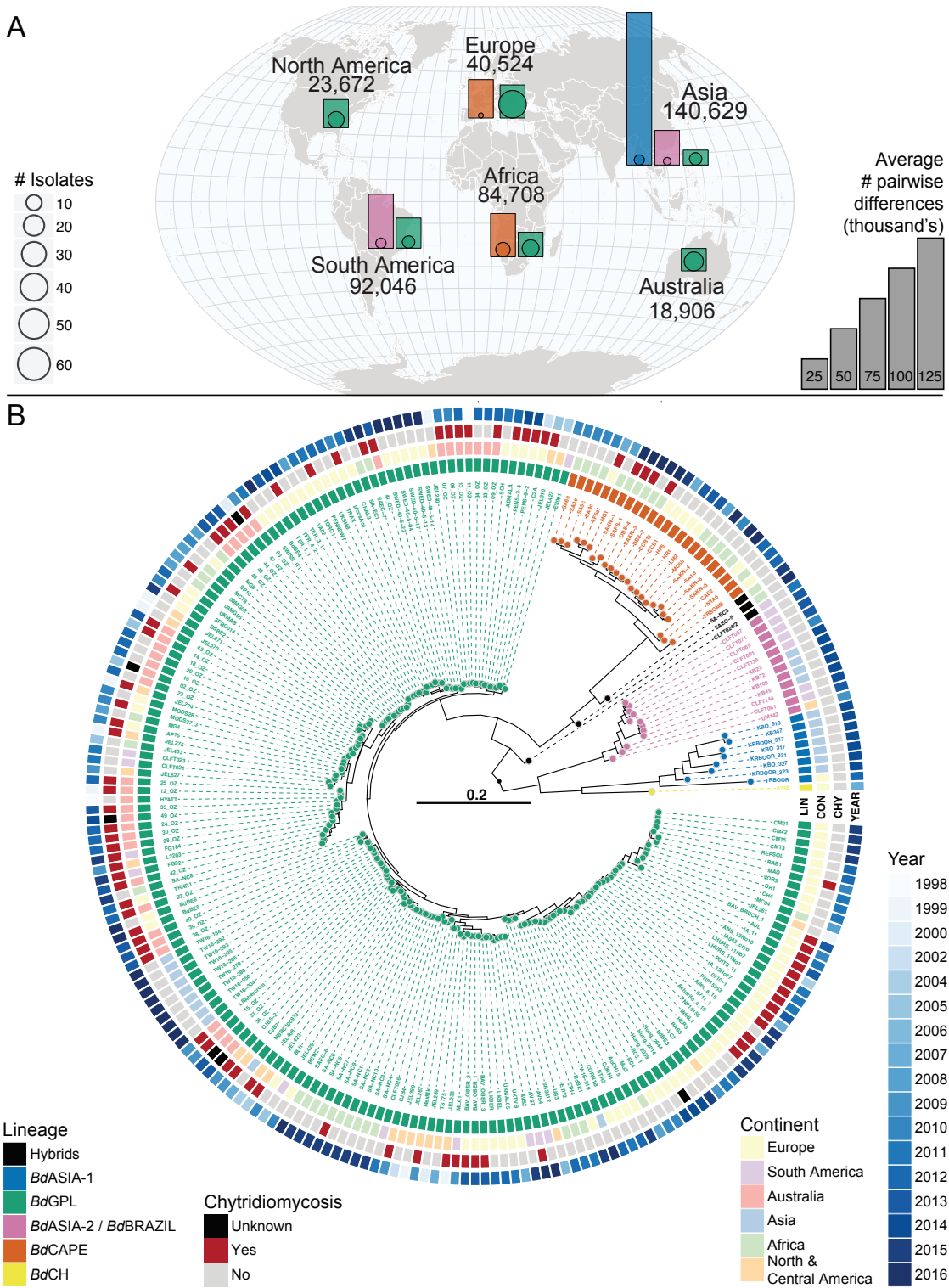
618 there is at least one homozygous difference between isolates. Average pairwise homozygous

619 segregating sites is the average number of sites with different homozygous genotypes

620 between all pairs of isolates within a lineage. Nucleotide diversity ( $\pi$ ) is the mean of the per-621 site nucleotide diversity. Tajima's  $D$  is reported as the mean over 1 kbp bins.

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623 **Figures:**



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625 **Fig. 1:** Genetic diversity and phylogenetic tree of a global panel of 234 *Batrachochytrium*

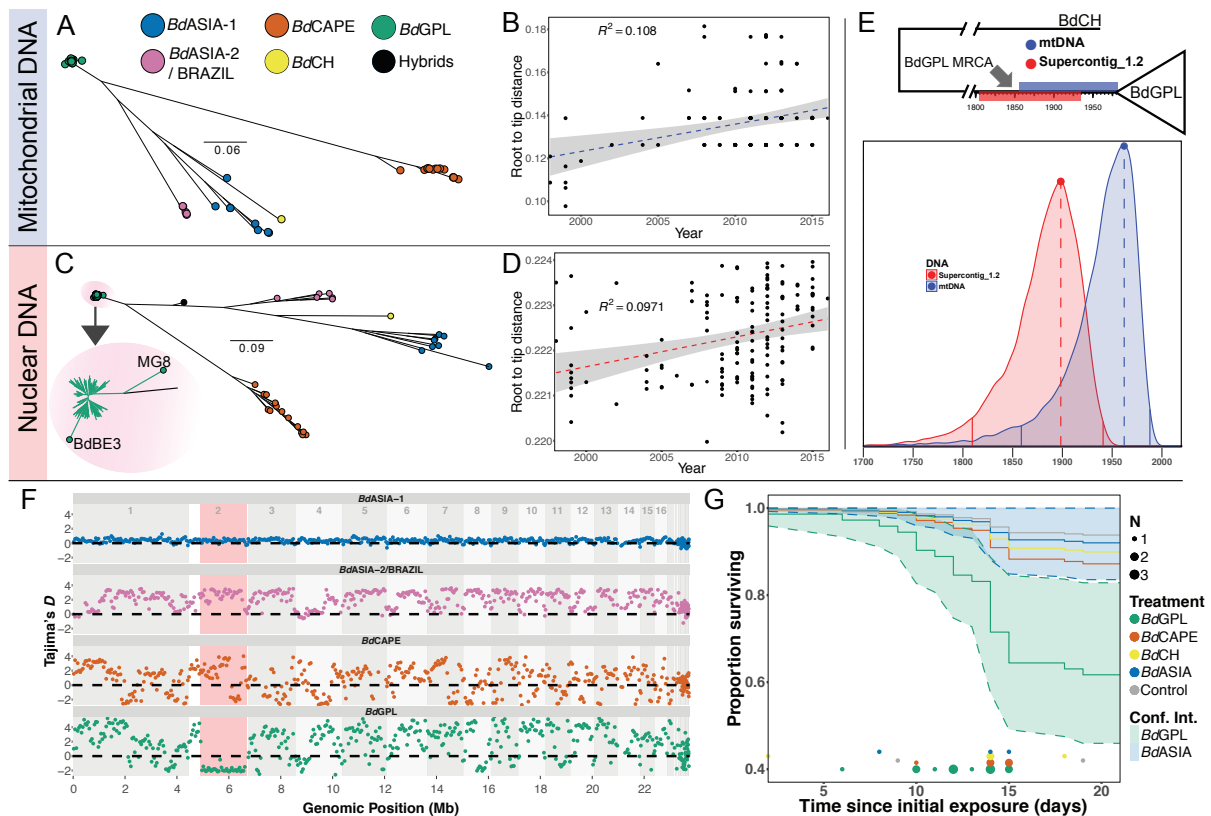
626 *dendrobatidis* isolates. **A.** Map overlaid with bar charts showing the relative diversity of

627 isolates found in each continent and by each major lineage (excluding isolates from traded

628 animals). The bar heights are the average number of segregating sites between all pairwise

combinations of isolates of each lineage in each continent (therefore only lineages with two or more isolates from a continent are shown). Outlined points at the base of each bar are scaled by the number of isolates for each lineage in that continent. The numbers around the outside of the globe are the average number of segregating sites between all pairwise combinations of isolates grouped by continent. Colours denote lineage as given by the legend in Fig 1B. **B.** Midpoint rooted radial phylogeny supports four deeply diverged lineages of *B. dendrobatidis*: *BdASIA-1*; *BdASIA-2/BdBRAZIL*; *BdCAPE* and *BdGPL*. All major splits within the phylogeny are supported by 100% of 500 bootstrap replicates. See Fig. S2 for tree with full bootstrap support values on all internal branches.



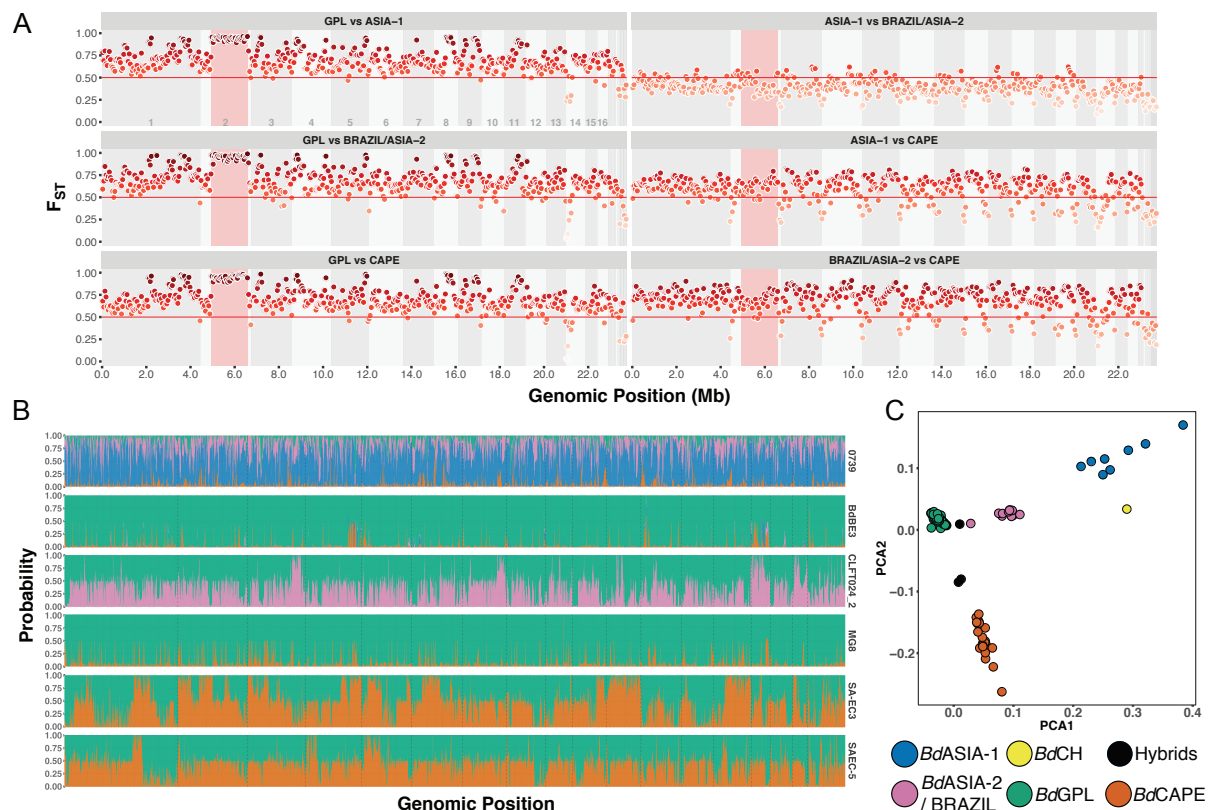


**Fig. 2:** Dating the emergence of *BdGPL*. **A.** Maximum likelihood (ML) tree constructed from 1,150 high quality SNPs found within the 178 kbp mitochondrial genome. **B.** Linear regression of root-to-tip distance against year of isolation for *BdGPL* isolates in mitochondrial DNA phylogeny in panel A, showing significant temporal trend (F-statistic = 14.35,  $p = 0.00024$ ). **C.** ML tree constructed from a 1.66 Mbp region of low recombination in Supercontig\_1.2. Two *BdGPL* isolates, *BdBE3* and *MG8* fall on long branches away from the rest of the *BdGPL* isolates (see inset zoom), due to introgression from another lineage (*BdCAPE*; see Fig. 3B) and were excluded from the dating analysis. **D.** Linear regression of root-to-tip distance against year of isolation for *BdGPL* isolates from phylogeny in panel C, with significant temporal trend (F-statistic = 15.92,  $p$ -value = 0.0001). **E.** Top figure shows *BdGPL* and outgroup *BdCH*, with the 95% HPD estimates for MRCA for *BdGPL* from mtDNA dating (blue) and nuclear DNA dating (red). Lower figure shows full posterior distributions from tip dating models for mtDNA (blue) and partial nuclear DNA (red) genomes. Solid vertical lines are limits of the 95% HPD. Dashed vertical lines denote the maximal density of the posterior distributions. **F.** Sliding 10 kb, non-overlapping window estimates of Tajima's D for each of the main *B. dendrobatidis* lineages. The region highlighted in red is the low recombination segment of Supercontig\_1.2. **G.** Survival curves for *Bufo bufo* metamorphs for different *B. dendrobatidis* treatment groups: *BdASIA-1* (blue); *BdCAPE* (orange); *BdCH* (yellow); *BdGPL* (green) and Control (grey). Confidence intervals

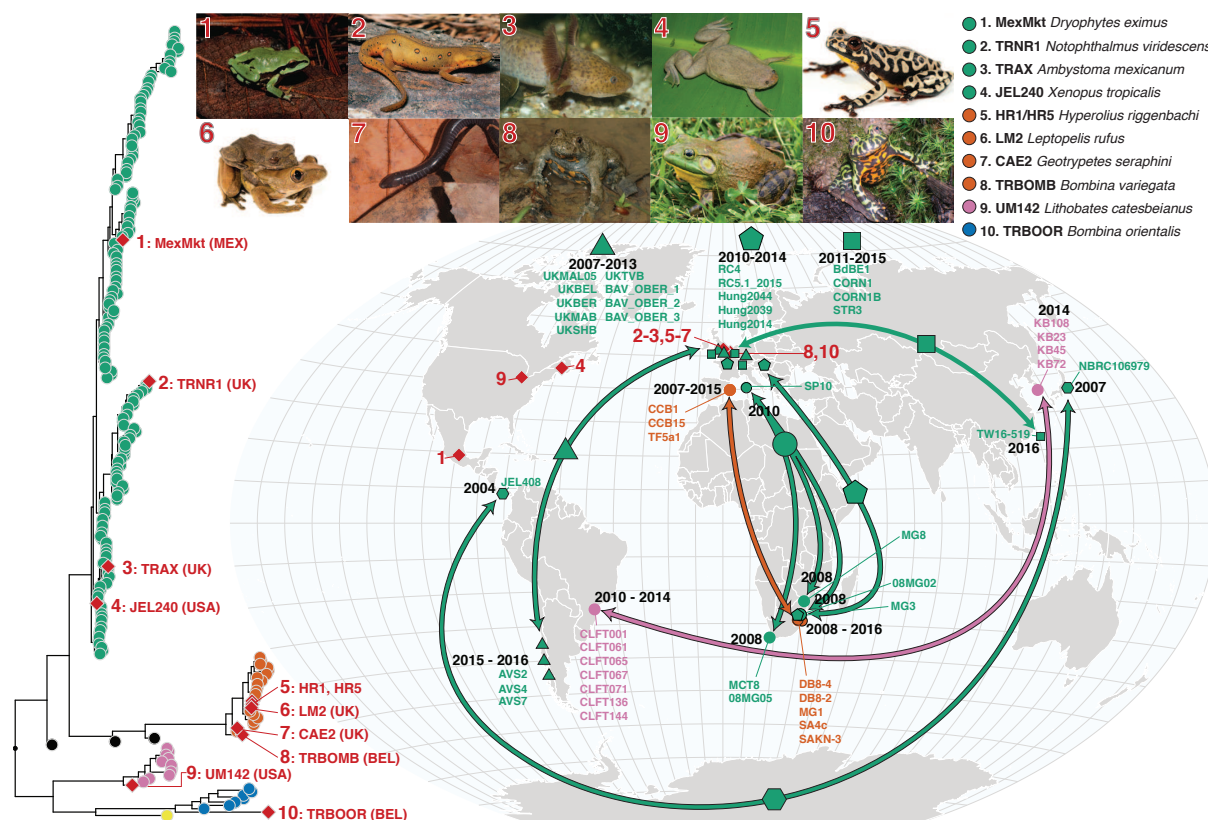
660 are shown for *Bd*GPL and *Bd*ASIA-1, showing no overlap by the end of the experiment.  
661 Instances of mortalities in each treatment group are plotted along the x-axis, with points  
662 scaled by number of mortalities at each interval (day).

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664



**Fig. 3:**  $F_{ST}$  and site-by-site STRUCTURE analysis. **A.** Non-overlapping, 10 kb sliding window of  $F_{ST}$  between lineages. The region highlighted in red is Supercontig\_1.2:500,000-2,160,000 low recombination region. **B.** Site-by-site analysis of population ancestry for a random selection of 9,905 SNPs. Results show those isolates found to be either hybrid (SA-EC3, SA-EC5 and CLFT024/2), or with significant introgression from non-parental lineages (isolates BdBE3 and MG8) or a chimera of un-sampled diversity, likely originating from East Asia (0739, the *BdCH* isolate). Each column represents a bi-allelic SNP position. The column is coloured according to the joint-probability of either allele copy arising from one of four distinct populations. Colours represent assumed parental lineages as given in Fig. 3C. **C.** Principle Components Analysis (PCA) of 3,900 SNPs in linkage equilibrium. Each point represents an isolate, coloured by phylogenetic lineage. The isolates separate into clearly defined clusters. The axes plot the first and second principle components.



**Fig. 4:** Genotypes of *Bd* isolated from infected amphibians in the international trade and phylogenetically linked genotypes from segregated geographic localities. The red diamonds on the phylogeny indicate isolates recovered from traded animals. Their geographic location is displayed by the red diamonds on the map. The red numbers link each trade isolate to the relevant picture of the donor host species atop the figure panel and their placement in the phylogeny. The arrows on the map link geographically separated isolates which form closely related phylogenetic clades with high bootstrap support ( $\geq 90\%$ ). Each clade is denoted by a different shape point on the map with the names of isolates within each clade displayed on the map. The dates displayed indicate the sampling time-frame for each clade. The phylogenetic position of each clade is displayed in Figs S10-14. The colours of points and arrows on the map indicate lineage according to the legend in Fig 1. A browsable version of this phylogeny can be accessed at <https://microreact.org/project/GlobalBd>. Photo credits: (1) *Hyla eximia* Ricardo Chaparro, (2) *Notophthalmus viridescens* Patrick Coin / CC-BY-SA 2.5, (3) *Ambystoma mexicanum* Henk Wallays, (4) *Xenopus tropicalis* Daniel Portik, (5) *Hyperolis riggenbachi* and (6) *Leptopelis rufus* Brian Freiermuth, (7) *Geotrypetes seraphini* Peter Janzen, (8) *Bombina variegata* and (9) *Rana catesbeiana* and (10) *Bombina orientalis* Frank Pasmans